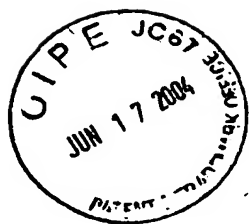


FIG. 1A



1 CGGACGCGTGGGCGCGCAGCCTGGCTGACCTGATCCTGGACCAGTGCCCCGACCGCGGGC 60
 61 CGCCGGTGCCGCGAGATGCTGGCCCAGCCGAGCGGCTGCTCTTCATCCTGGACGGCGCGG 120
 1 M I A Q P Q R L I F I L D G A D 16
 121 ACGAGCTGCCGGCGCTGGGGGGCCCCGAGGCCGCGCCCTGCACAGACCCCTTCGAGGCGG 180
 17 E L P A L G G P E A A P C T D P F E A A 36
 181 CGAGCGGCGCGCGGGTGCTAGGCGGGCTGCTGAGTAAGGCGCTGCTGCCCACGGCCCTCC 240
 37 S G A R V I G G I I S K A L I P T A L L 56
 241 TGCTGGTGACACGCGCGCCGCCCGCCCCGGGAGGCTGCAGGGCCGCTGTGTTCCCCGC 300
 57 I V T T R A A A P G R I Q G R L C S P Q 76
 301 AGTGCGCCGAGGTGCGCGGCTTCTCCGACAAGGACAAGAAGAAGTATTTCTACAAGTTCT 360
 77 C A E V R G F S D K D K K K Y F Y K F F 96
 361 TCCGGGATGAGAGGAGGGCCGAGCGCGCTACCGCTTCGTGAAGGAGAACGAGACGCTGT 420
 97 R D E R R A E R A Y R F V K E N E T I F 116
 421 TCGCGCTGTGCTTCGTGCCCTTCGTGTGCTGGATCGTGTGCACCGTGCTGCGCCAGCAGC 480
 117 A I C F V P F V C W I V C T V I R Q Q L 136
 481 TGGAGCTCGGTCGGGACCTGTGCGGCACGTCCAAGACCACCACGTACGTGTACCTGCTTT 540
 137 E L G R D L S R T S K T T T S V Y I L F 156
 541 TCATCACCAGCGTTCTGAGCTCGGCTCCGGTAGCCGACGGGCCCCGGTTGCAGGGCGACC 600
 157 I T S V L S S A P V A D G P R L Q G D I 176
 601 TGC GCAATCTGTGCCGCTGGCCCCGCGAGGGCGTCCTCGGACGCAGGGCGCAGTTTGCCG 660
 177 R N I C R I A R E G V L G R R A Q F A E 196
 661 AGAAGGAACCTGGAGCAACTGGAGCTTCGTGGCTCCAAAGTGCAGACGCTGTTTCTCAGCA 720
 197 K E I E Q L E L R G S K V Q T L F L S K 216
 721 AAAAGGAGCTGCCGGGCGTGCTGGAGACAGAGGTCACCTACCAGTTCATCGACCAGAGCT 780
 217 K E L P G V L E T E V T Y Q F I D Q S F 236
 781 TCCAGGAGTTCCTCGCGGCACTGTCTACCTGCTGGAGGACGGCGGGGTGCCAGGACCG 840
 237 Q E F L A A L S Y L I E D G G V P R T A 256
 841 CGGCTGGCGGCGTTGGGACACTCCTGCGTGCGGACGCCAGCCGCACAGCCACTTGGTG 900
 257 A G G V G T L I R G D A Q P H S H L V L 276



D0066 NP

2/16

FIG. 1B

901 TCACCACGCGCTTCCTCTTTCGGACTGCTGAGCGCGGAGCGGATGCGCGACATCGAGCGCC 960
277 T T R F L F G U L S A E R M R D I E R H 296

961 ACTTCGGCTGCATGGTTTCAGAGCGTGTGAAGCAGGAGGCCCTGCGGTGGGTGCAGGGAC 1020
297 F G C M V S E R V K Q E A L R W V Q G Q 316

1021 AGGGACAGGGCTGCCCCGGAGTGGCACCAGAGGTGACCGAGGGGGCCAAAGGGCTCGAGG 1080
317 G Q G C P G V A P E V T E G A K G L E D 336

1081 ACACCGAAGAGCCAGAGGAGGAGGAGGAGGGAGAGGAGCCCACTACCCACTGGAGTTGC 1140
337 T E E P E E E E E G E E P N Y P L E L U 356

1141 TGTACTGCCTGTACGAGACGCAGGAGGAGCGCTTTGTGCGCCAAGCCCTGTGCCGTTCC 1200
357 Y C U Y E T Q E D A F V R Q A L C R F P 376

1201 CGGAGCTGGCGCTGCAGCGAGTGCCTTCTGCCGCATGGACGTGGCTGTTCTGAGCTACT 1260
377 E L A L Q R V R F C R M D V A V L S Y C 396

1261 GCGTGAGGTGCTGCCCTGCTGGACAGGCACTGCGGCTGATCAGCTGCAGATTGGTTGCTG 1320
397 V R C C P A G Q A L R U I S C R L V A A 416

1321 CGCAGGAGAAGAAGAAGAGCCTGGGGAAGCGGCTCCAGGCCAGCCTGGGTGGCGGCA 1380
417 Q E K K K K S U G K R L Q A S L G G G S 436

1381 GTTCTCAAGGCACCACAAAACAAGTCCAGCCTCCCTTCTTCATCCACTCTTTCAGGCAA 1440
437 S Q G T T K Q U P A S L L H P L F Q A M 456

1441 TGA CTGACCCACTGTGCCATCTGAGCAGCCTCACGCTGTCCCACTGCAA ACTCCCTGACG 1500
457 T D P L C H U S S L T L S H C K L P D A 476

1501 CGGTCTGCCGAGACCTTTCTGAGGCCCTGAGGGCAGCCCCGCACTGACGGAGCTGGGCC 1560
477 V C R D L S E A U R A A P A L T E U G U 496

1561 TCCTCCACAACAGGCTCAGTGAGGCGGGA CTGCGTATGCTGAGTGAGGGCCTAGCCTGGC 1620
497 L H N R L S E A G L R M U S E G L A W P 516

1621 CGCAGTGCAGGGTGCAGACGGTCAGGGTACAGCTGCCTGACCCCAGCGAGGGCTCCAGT 1680
517 Q C R V Q T V R V Q L P D P Q R G L Q Y 536

1681 ACCTGGTGGGTATGCTTCGGCAGAGCCCCGCCCTGACCACCTGGATCTCAGCGGCTGCC 1740
537 U V G M U R Q S P A U T T L D U S G C Q 556

1741 AACTGCCCCGCCCCATGGTGACCTACCTGTGTGCACTCCTGCAGCACCAGGGATGCGGCC 1800
557 U P A P M V T Y U C A V U Q H Q G C G U 576



D0066 NP

3/16

FIG. 1C

1801 TGCAGACCCTCAGTCTGGCCTCTGTGGAGCTGAGCGAGCAGTCACTACAGGAGCTTCAGG 1860
577 Q T S A S V E S E Q S L Q E Q A 596

1861 CTGTGAAGAGAGCAAAGCCGGATCTGGTCATCACACACCCAGCGCTGGACGGCCACCCAC 1920
597 V K R A K P D V I T H P A L D G H P Q 616

1921 AACCTCCCAAGGAACTCATCTCGACCTTCTGAGGCTCTGGTGGCCAGAGCAGGGTGAAG 1980
617 P P K E L I S T F 625

1981 ACCCTAGTCAAAGTCCCTGTGGAGAGAACGGCCCATTCOAAGGGCAGGAGGATATTGCTC 2040

2041 TCGGCCTTTGGGAAACTTTTGAGCCGAGAGGCCGAGACAGGCATGTGGGAGGCCAGAC 2100

2101 ACGGCACCCTGCCCCGTCCAGGACAGGCCAGGACCTGCCCTCTCTCCACACCTGGGGT 2160

2161 ACCCCTTCTCCCCAGCCCCACCACTACTCCACCCACCTTCTCTCCTGAGACCCTCCAG 2220

2221 CCATTCCCCTTGAAAAACCCCCGACCCCAAGCCACAATAATGACAGCGAGAGCTCCAA 2280

2281 TTAATAAGCACCTACCTGGCGGCAGAATAACCCTTCACTGCCTGATCCCCATCTGCAGT 2340

2341 GTGGCCCAACAGCCCCCAGAACTATGCCACATAGACTGGAGGTAGGCAGTTCACCGTCC 2400

2401 CTCCCTGTTAGGAATGAGACCATCCCTGAGGCTATGGCCAGGCCACAGGCGTCCAGTG 2460

2461 TCTGAGATCTTTGGGAAGGGAGACTAGGGCAGGTGGAGACAGCGCAGAACCCCGTGCTG 2520

2521 GGTGGGAAGCATGACCACATGGTGGGTGAGCAGCCCCATGCACTGACGGTAAATTCCCC 2580

2581 TGTGGACTCATTCTGTGTTGTTTCTATTACACCTGGCCAGGCGTGGTACAATACAGGTCG 2640

2641 GTGCTCACAAA 2689

FIG. 2A-1

		1		50
HLRRSI1		(1)	-----	
caspase_recruitment_protein		(1)	MAGGAWGR L ACYLEFL L KK E ELKEF O LLANKA H SRSSSGET P AQ P EK T SG	
cryopyrin		(1)	-MASTRCK L ARYLED L EDV D LKKFK M HLED V PP O KGCIP L PRG O TEKADH	
Nucleotide_Binding_site		(1)	---MGFN L QALL E Q L LSQ D EL S KFKY L IT T ESPA H ELQ K TPH K EV D KADG	
		51		100
HLRRSI1		(1)	-----	
caspase_recruitment_protein		(51)	MEVAS L VAQYCE Q RAW D LALH T WE Q MGLR S LCA Q AQ E GAGH S PSFP Y SP	
cryopyrin		(50)	V D L A TL M IDFN G EE K AWA M AM W IFAA T NR R DL V E K AK R DEPK W CS D NARV	
Nucleotide_Binding_site		(47)	K Q LVE F IL T THC D SYW V EMAS L QV F E K MHR M DLSE R AK D EVREA L KS F ENK	
		101		150
HLRRSI1		(1)	-----	
caspase_recruitment_protein		(101)	SEPHLGSPSQPTSTAVLMPWIHELPA G CTQGSERRVLRQLPDTSGRRWRE	
cryopyrin		(100)	SN-----	
Nucleotide_Binding_site		(97)	RK-----	



FIG. 2A-2

	151		
HLRRI1	(1)	-----	200
caspase_recruitment_protein	(151)	ISASHLYQALPSSPDHESPSPQESNAPTSTAVLGSWGSPQP	PSIAPREQE
cryopyrin	(102)	-----	PVTCQEDS
Nucleotide_Binding_site	(99)	-----	PLSLGITR-
	201		250
HLRRI1	(1)	-----	
caspase_recruitment_protein	(201)	APGTQWPLDETSGIYYTEIREREREKSEKGGPPMAAVVGITPPQAHSSIQP	
cryopyrin	(111)	IEEWMGLLEYLEYLSRISICKMKDYRKKYVRSRFQCIEDRNARLGESV	
Nucleotide_Binding_site	(107)	KERPPEDVDVDEMLERFKTEAQDKDNRCRYILKTKEREMWKSWPGDSKEVQV	
	251		300
HLRRI1	(1)	-----	
caspase_recruitment_protein	(251)	HHHPWEPSVRESLCSTWPWKNEDEFNQKFTQLLLQRP	PHPRSQDPLVKRSW
cryopyrin	(161)	SLNRYTRRLRIKEHRSQQEREQELLAIGKTKTCESPV	-----
Nucleotide_Binding_site	(157)	MAERXKMLIPFSNPR	-----



FIG. 2A-3

HLRRSI1	301		
caspase_recruitment_protein	(1)	---	350
cryopyrin	(301)	PDVVEENRGHIEIRDLFPGGLDQEPRIIVLQGAAGIGKSTLARQVKEA	
Nucleotide_Binding_site	(199)	-----SPKMELLFDPDDEHSEPVHTVVFQGAAGIGKTIILARKMMLD	
	(172)	-----VLPGPFSYTVVLYGPAAGLGKTTLAQKLMLD	
HLRRSI1	351		400
caspase_recruitment_protein	(1)	---	MLA
cryopyrin	(351)	WGRGQLYGDRFQHVFFYFSCRELAQSKVVSIAELIGKDCGTATPAPIRQILS	
Nucleotide_Binding_site	(241)	WASGILYQDRFDYLFYTHCREVSLVTQRSIGDLIMSCCPDPNPPHKTIVR	
	(202)	WAEENLIHK-FKYAFYLSCRELSRLGPCSFAELVFRDWPELQDDIPHILA	
HLRRSI1	401		450
caspase_recruitment_protein	(4)	QPQRLLFILDGADLP-ALGCPPEAAPCTDPPFAASGARVLCGLLSKALLP	
cryopyrin	(401)	RPERLLFILDGVDEPCWVLQEPSELCLHNSQPQPADALLGSLIGKTIIP	
Nucleotide_Binding_site	(291)	KPSRI LFLMDGFDELQCAFEDEHICPLCTDWQKAERGDI LLSLIRKKLLP	
	(251)	QARKK LFWIDGFDELGAAPGALIEDICGDWEKKKFPVPLIGSLINRVMLP	



FIG. 2A-4

		451			500
HLRRSI1		(53)	TALLVTTTRAAAPCRLOGRICSPQAEVRGFSDDKDKKKYFYKFFRDERRA		
caspase_recruitment_protein		(451)	EASLLTARTTALQNLIPSLQARWVEVLGFSESSRKEYFYRYFTDERQA		
cryopyrin		(341)	EASLLITTRPVALEKLOHLIDHPRHVEILGFSEAKRKEYFFKYSDEAQA		
Nucleotide_Binding_site		(301)	KAALLVTTTRPRALRDLRLILAEETPIYRVEGFLEEDKRAYFLRHFCGEDEQA		
		501			550
HLRRSI1		(103)	ERAYRIVKENETLFALCFVPEVCWIVCTVLRQQLELGRDLSRTSKTTTTSV		
caspase_recruitment_protein		(501)	TRAFRLVKSNEKELWALCTVPWVSWLACTCLMQQMKRKEKLTILTSKTTTTL		
cryopyrin		(391)	RAAFSLIOENEVLFATMCFHPLVCWIVCTGLKQQMESGKSLAQTSKTTTAV		
Nucleotide_Binding_site		(351)	MRAFELMRSNAALFQLGSAPAVCWIVCTILKLQMEKGEDPVPITCLTRTGL		
		551			600
HLRRSI1		(153)	YLLFITSVLSSAPVADGCPRLQCDLRNLCRLAREGVLCRRQAFAEKELQOL		
caspase_recruitment_protein		(551)	CLHMLAQALQAP-----LGPQLRDLCSLAAEGIWQKTLFSPDDIRKH		
cryopyrin		(441)	YVFFLSSLQPRGGSQEHGLCAHLWGLCSLAAADGIWNNOKILFFESDLRNH		
Nucleotide_Binding_site		(401)	FLRFLCSREP-----QCAQLRCALRTLSSLAAQGLWAQTSVTHREDIERL		



FIG. 2B-1

		601				650
HLRSI1		(203)	ELRCSKVQITLFLSKKELPGVLETEVTYQFIDQSFQEFLLAALSYLEDDGGV			
caspase_recruitment_protein		(595)	GLDCAITSTFLKMG--ILQEHPIPLSYSFIHLQFQEFFAAMSYLEDEK-			
cryopyrin		(491)	GLOKADVSNFLRMN-LEQKEVDGEKFYSFIHMTFQEFFAAMYILLEEKE			
Nucleotide_Binding_site		(446)	GVOESDRLFLDGD-ILRQDRVSKGCYSFIHLSFQQLTALFYTLEKEEE			
		651				700
HLRSI1		(253)	PRTAAGC-----VGTLLRCDAQPHSHLMLTTRFLFGLLSAERMMD			
caspase_recruitment_protein		(642)	-----GRGKHSNCIIDLLEKTLFAYGTHGLFGASTTTRFLTGLISDEGERE			
cryopyrin		(540)	GRTNVPGSRLEKLP SRDVTLLLENYCKFEKGYLIFVWRFLFGLVNOERTSY			
Nucleotide_Binding_site		(495)	EDRDGHTWDIG----DVQKLISGVERLRNPDLIQAGYYSFGLANERAKKE			
		701				750
HLRSI1		(293)	IERHFGCMVSEPVKQEA LRWVQCGQGCGPGVAPEVTEGAKGLEDTTEEPPEE			
caspase_recruitment_protein		(686)	MENIFHCRLSQ--GRNLMQWVPSL-----QLLQPHS-----			
cryopyrin		(590)	LEKLSCKISQOIRLELLKWI EVK-----AKAKKLQIQPSQ			
Nucleotide_Binding_site		(541)	LEATFGCRMSPDIKQELLRCDISC-----KCGHSTVTDLQ			



751 800

FIG. 2B-2

751
(343) EEEGEEPNYP LELLYCLYETQEDAFVROATCRFPE LALQ RVRFRCMDVAV 800
(716) ----- LESLECLYETRNKTHLTQWAEFEEMCMC -- VETDMELLV
(626) ----- LELFYCLYEMQEEEDFVQRAMDYFPKIEEN -- LSTRMDHMV
(576) ----- ELLGCLYESQEEELVKEWAFKEISLEH -- LNAVVDVVP

801
(393) L S M C V R C C P A Q A L R L I S C R L V A A Q E K K K K S L C K R L Q A S L C G G S S Q ---
(754) C T F C I K F S R H V K K L Q L I E G R O H R S T W S P S M V L F R W P V T D A Y W Q I L F S -
(664) S S F C I E N C H R V E S L S I G F L T H N M P K E E E E E K E C R H L D M V C V L P S S S E A A
(612) S S F C V K H C R N L O K M S L Q V I K E N L P E N V T A S E S D A E V E R S O D D O H M L P F W T 850

851
(439)-----
(803)-----
(714) CSHGIVN\$H-----
(662) DLCSIFG\$NKDLMGLAINDSFLSASLVRILCEQIASDTC\$H\$R\$VV\$F\$K\$N\$T\$S\$-----
900

10/16

FIG. 2B-3

		901			950			
HLRRSI1		(439)	-----	GIITKQLPASL	EEHELFOAMTDPLCELSSLT			
caspase_recruitment_protein		(803)	-----	VLKVIIRNLK	EELDLSGNSLS	SESAVKS	LC	KTTLRRPRCLLETLR
cryopyrin		(725)	SSFCRGLF	SVLSTQS	LTELDLSNLS	GDP	GMRVLCETLQHPGCNIRRLW	
Nucleotide_Binding_site		(712)	PADAHRNL	CLALRCH	TKTVTYLT	LTQGNDDMF	PALCEVLRHPECNLRVLG	
HLRRSI1		951			1000			
caspase_recruitment_protein		(468)	LSHCKLP	DAVCRDL	SEALRAAP	ALTELC	LLFNRLSEAGLRMLSEGLAWPQ	
cryopyrin		(844)	LACGLT	AEDCKDL	AFGLRANQ	LTELDLS	FNVLMDAGAKHLCQRLRQPS	
Nucleotide_Binding_site		(775)	LGRCL	SHCCFD	DISIVL	SSNQKL	VELDLSDNALGDFGIRLLCVGLKHL	
		(762)	LVSCS	ATTQ	QWADLS	ALAEV	NQSLTCAVNLSDNELDEGAKLLYTTLRHPK	
HLRRSI1		1001			1050			
caspase_recruitment_protein		(518)	CRVQTV	RVQLPDPQ	-RGLQYLV	CMRLRQ	SPALTTLDLSCCQLPAPMVTYLC	
cryopyrin		(894)	CKLQRL	QLVSCGL	TSDCCQDLASVLS	ASPSLKELDLQNNLDDVGVRLC		
Nucleotide_Binding_site		(825)	CNLK	KLWLVSC	CLTSACCQDLASVLS	TSLSLRLYV	GENALGDSGVAILC	
		(812)	CFLQRL	SLSEN	CHLT	EANC	CKDLAAVIVVSR	ELTHLCLAKNPICNTGVKELC



11/16

FIG. 2B-4

HLRRSI1	1051	1100
caspase_recruitment_protein	(567) AVLQHQC	AVLQHQC
cryopyrin	(944) EGLRHPACKLIRLGLD	EGLRHPACKLIRLGLD
Nucleotide_Binding_site	(875) EKA	EKA
	(862) EGLRYPECKLQTLVLMN	EGLRYPECKLQTLVLMN
HLRRSI1	1101	1150
caspase_recruitment_protein	(617) PPKELISTF	PPKELISTF
cryopyrin	(994) PIEGLDTGEMSNSTSL	PIEGLDTGEMSNSTSL
Nucleotide_Binding_site	(925) KGI	KGI
	(912) KGM	KGM
HLRRSI1	1151	1200
caspase_recruitment_protein	(626) ---	---
cryopyrin	(1044) AEFSSPEVVPVELT	AEFSSPEVVPVELT
Nucleotide_Binding_site	(975) GNN	GNN
	(961) GON	GON





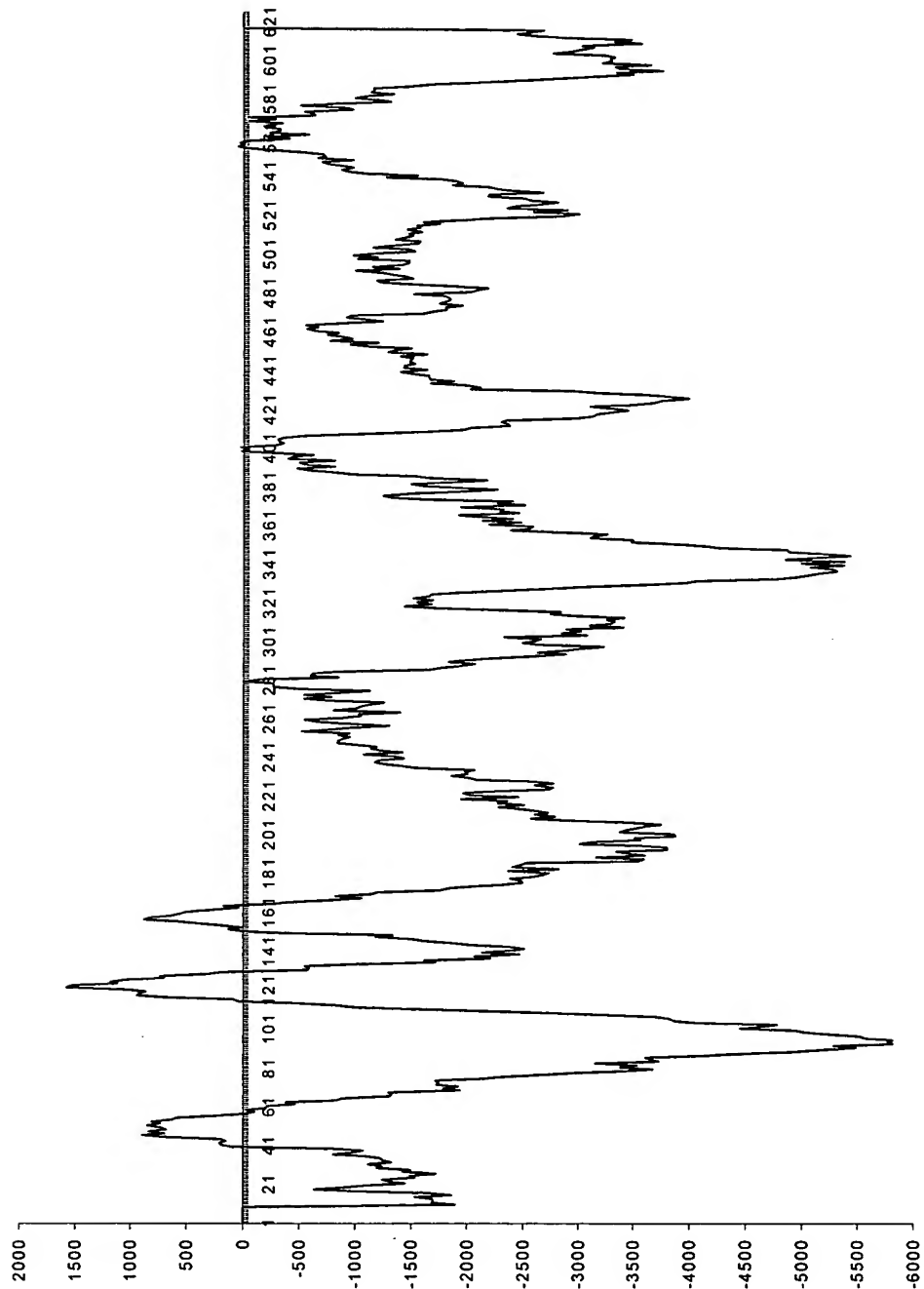
HLRRSI1	(626)	-----	1201	1250
caspase_recruitment_protein	(1094)	EKNLYRVHFPVAGSRRWPNITGLCFVWREAVTVEIEFCVWDQFLGEINPQH		
cryopyrin	(1022)	EKPELTIVVEFPSW		
Nucleotide_Binding_site	(1008)	KNPQLIITDTEKHHPWAEERPSSHDFEML		
			1251	1300
HLRRSI1	(626)	-----		
caspase_recruitment_protein	(1144)	SWMVAGPLLDIKAEPGAVEAVHLPHFVALQGGHVDTSLFQVAHFKEEGML		
cryopyrin	(1035)	-----		
Nucleotide_Binding_site	(1034)	-----		
			1301	1350
HLRRSI1	(626)	-----		
caspase_recruitment_protein	(1194)	LEKPARVELHHIVLENPSPLGVLLKMIHNALRFIPVTSVVLVYHRLHP		
cryopyrin	(1035)	-----		
Nucleotide_Binding_site	(1034)	-----		

13/16

FIG. 2C-2

HLRRSI1	1351		1400
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1244)	EEVTFHLYLIPSDCSIRKELELCYRSPGEDQLFSEFYVGHLSGIRLQVK	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1401		1450
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1294)	DKKDETLVWEALVKGDLMPATTLIPPACIAVSPPLDAPQLLHFVDQYRE	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1451		1500
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1344)	QLIARVTSVEVVLDKLGQVLSQEYQYERVLAEENTRPSQMRKLFSLSQSWD	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----
HLRRSI1	1501		1536
caspase_recruitment_protein	(626)	-----	-----
cryopyrin	(1394)	RKCKDGLYQALKETHPHLIMELWEKSKKGLPLSS	
Nucleotide_Binding_site	(1035)	-----	-----
	(1034)	-----	-----

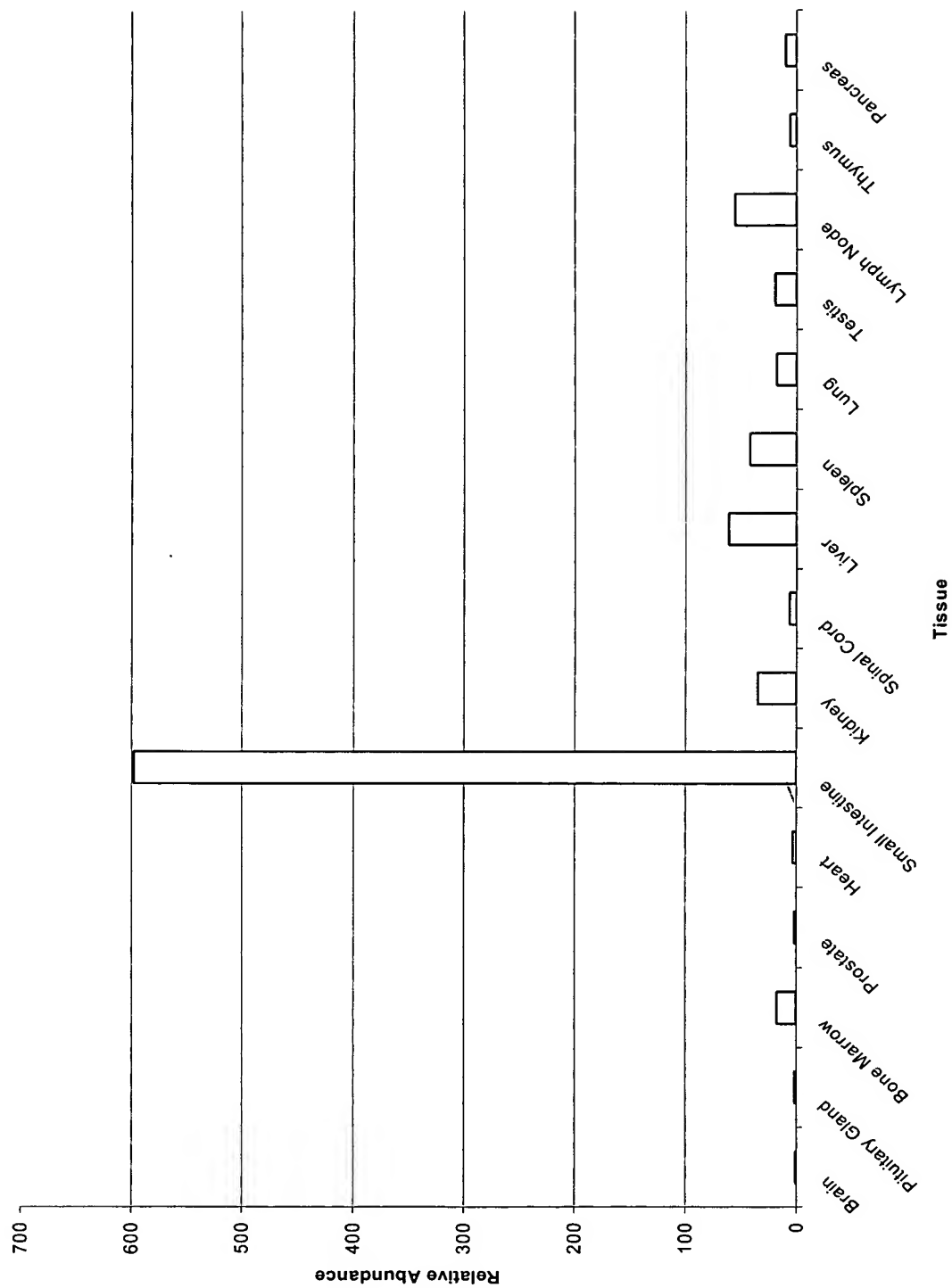




D0066 NP

15/16

FIG. 4





D0066 NP

16/16

FIG. 5

Protein	Genbank ID	Identities	Similarities
human caspase recruitment protein 7	gi 10198209	36.3%	44.0%
human nucleotide binding site protein	gi 10198207	35.0%	42.2%
human cryopyrin protein	gi 17027237	35.7%	46.0%